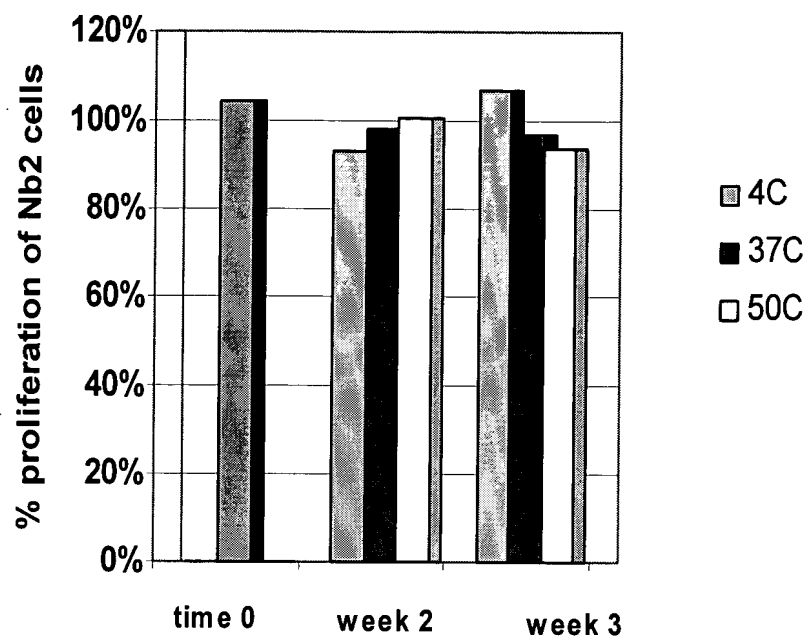
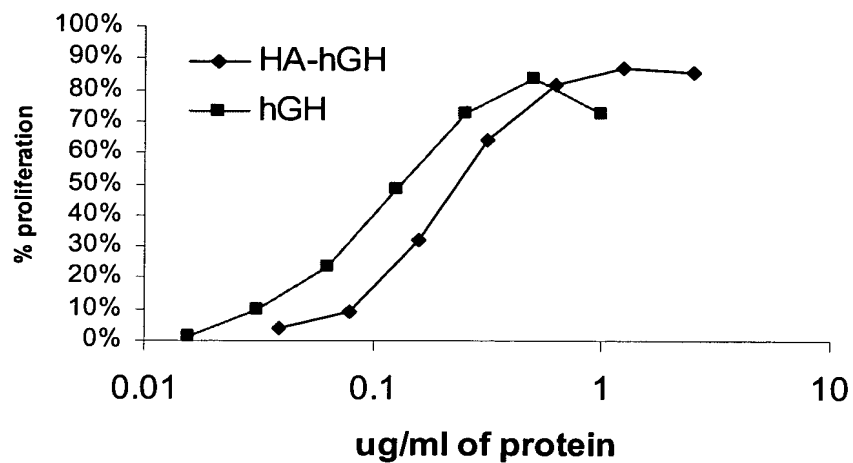


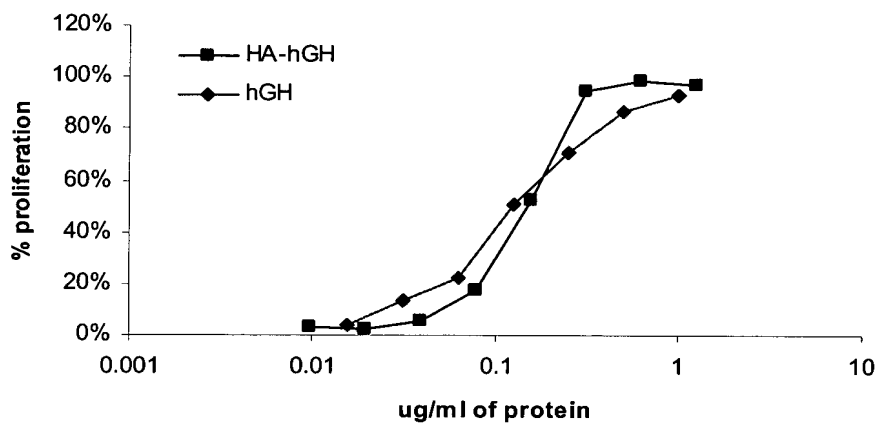
**Figure 1**



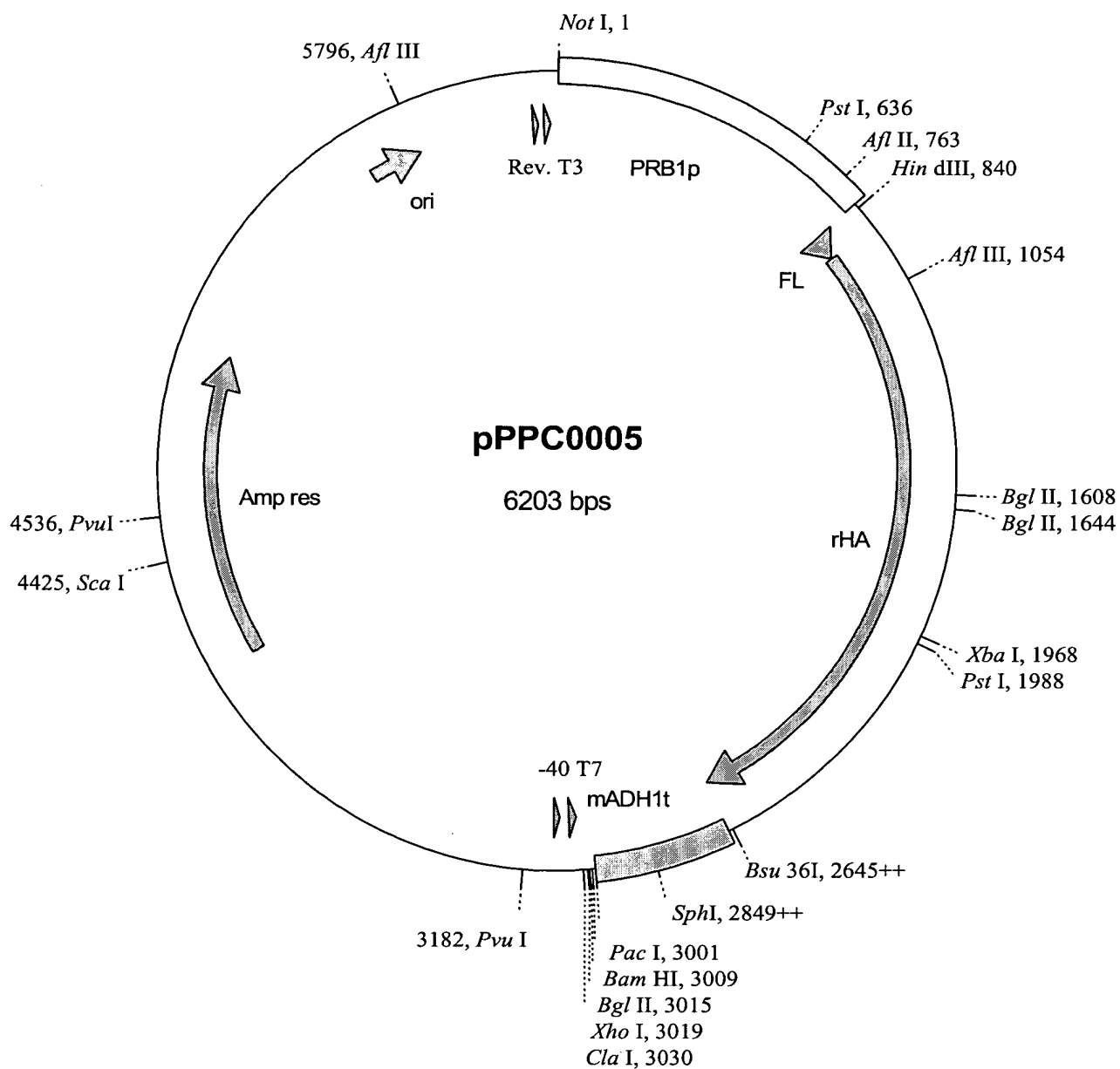
**Figure 2**



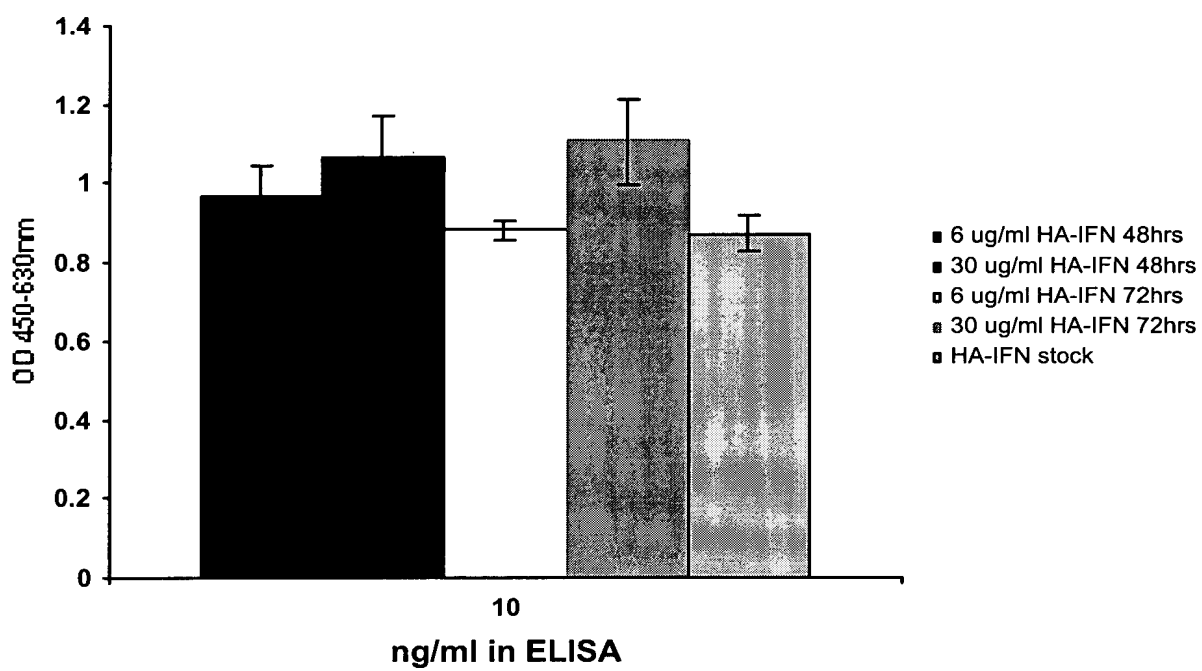
**Figure 3A**



**Figure 3B**

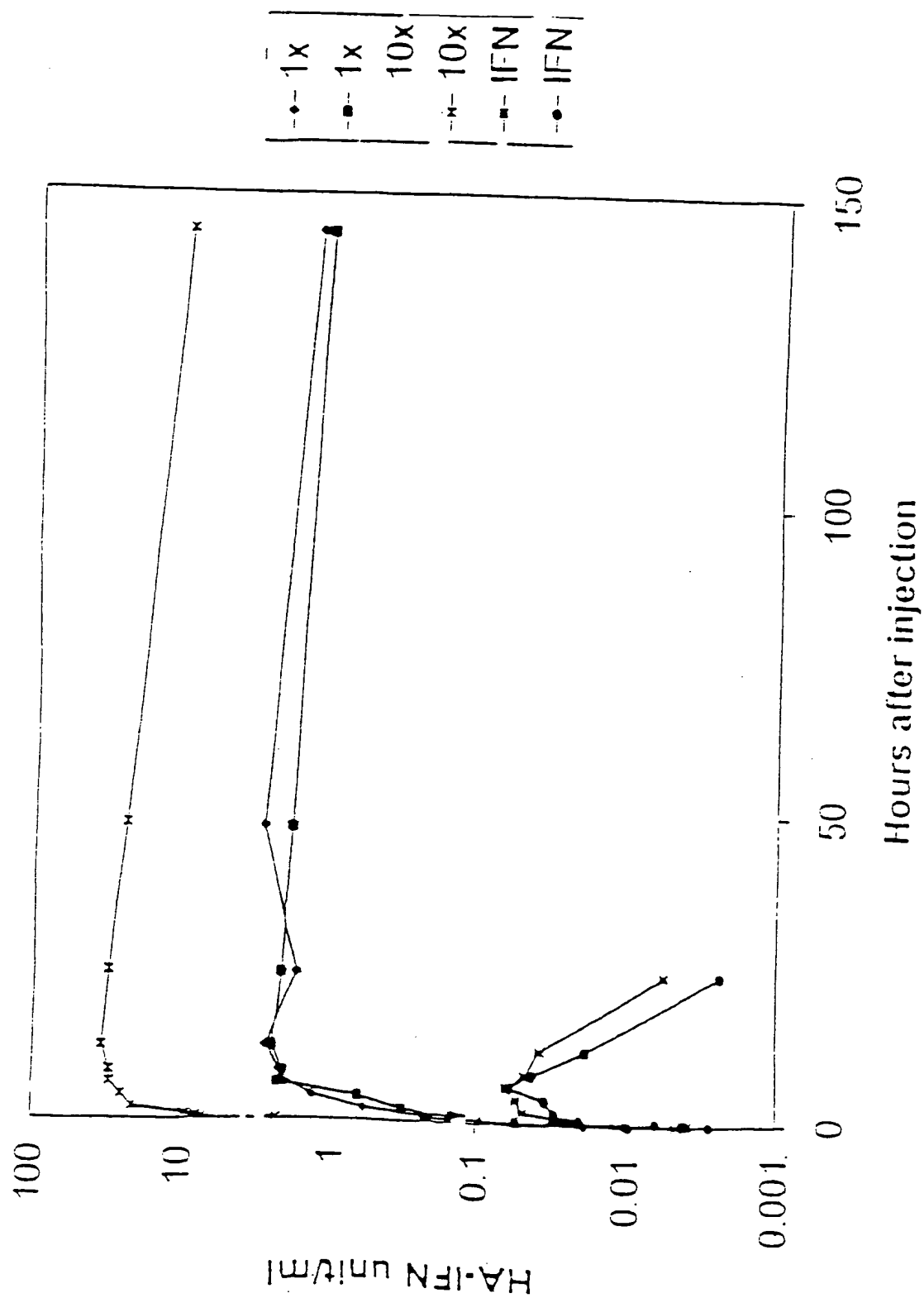


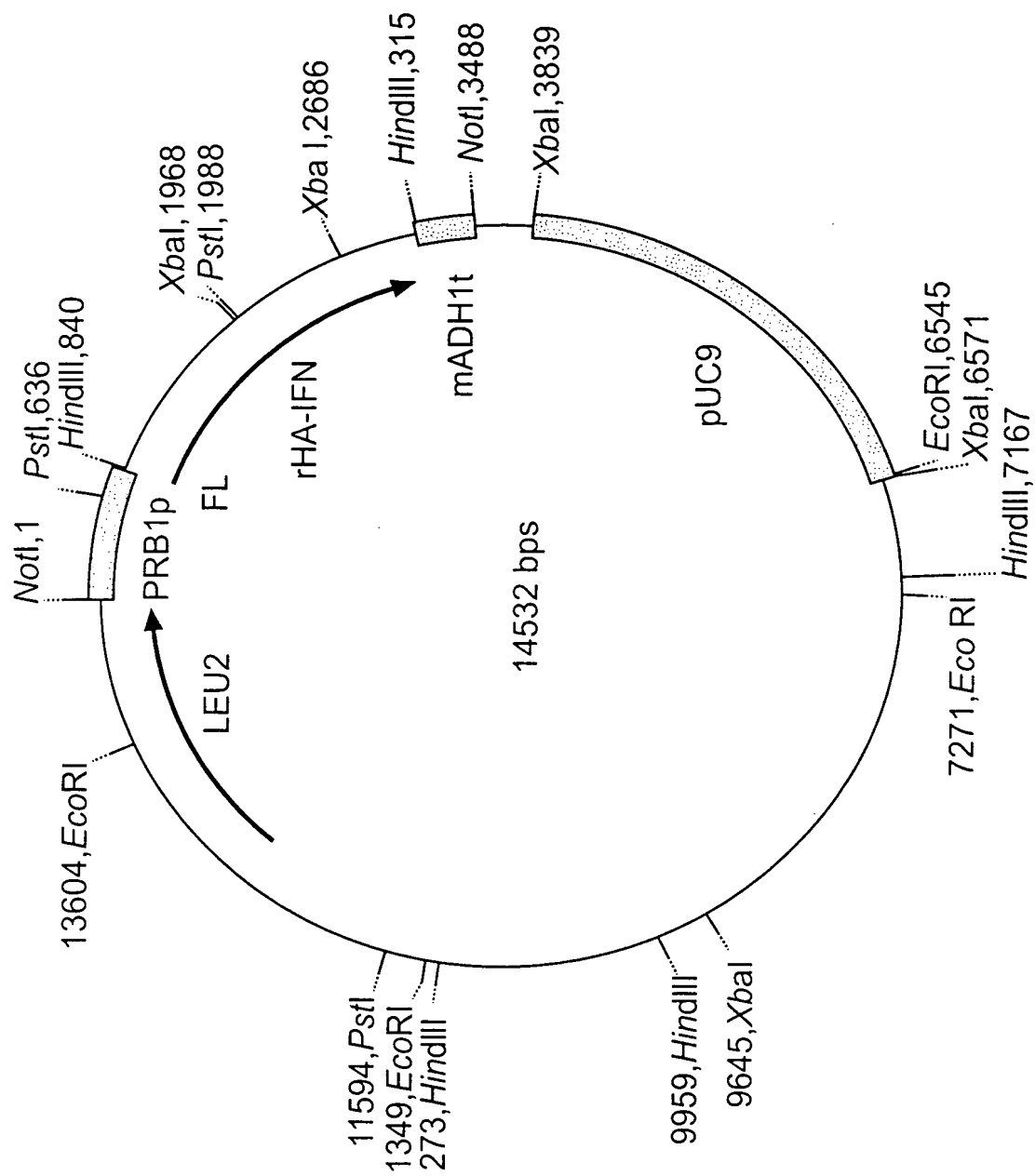
**Figure 4**



**Figure 5**



[illegible]



**FIG. 8**



# Figure 9

```

1    DAHKSEVAHR FKDLGEENFK ALVLIAFAQY LQQCPFEDHV KLVNEVTEFA
      HHHHH HHH      HHH HHHHHHHHHHH      HHHHH HHHHHHHHHHH

51   I          II          III
      KTCVADESAE NCDKSLHTLF GDKLCTVATL RETYGEMADC CAKOEPERNE
      HHHHH      HHHHH HHHHH      HHHH H      HHHH

101  CFLQHKDDNP NLPRLVRPEV DVMCTAFHDN EETFLKKYLY EIARRHPYFY
      HHHH      H      HHHHHHHHH      HHHHHHHHH HHHHH

151  IV
      APPELLFFAKR YKAAFTECCO AADKAACLLP KLDEL RDEGK ASSAKQRLKC
      HHHHHHHHHHH HHHHHHHHH      HHHHH HHHHHHHHHHH HHHHHHHHHHH

201  V
      ASLQKFGERA FKAWAVARLS QRFPKAEFAE VSKLVTDLTK VHTECCHGDL
      HHHHH      HH HHHHHHHHHHH HH      HHH HHHHHHHHHHH HHHHH      HH

251  VI          VII
      LECADDRADL AKYICENODS ISSKLKECCE KPILLEKSHCI AEVENDEMPA
      HHHHHHHHHHH HHHHH      HHHHH      HHHHHHH H

301  DLPSLAADFV ESKDVCKNYA EAKDVFLGMF LYEYARRHPD YSVVLLLRLA
      HHHH      HHHHHH      HHHHHHH HHHHHH      HHHHHHHH

351  VIII
      KTYETTLEKC CAAADPHECY AKVFDEFKPL VEEPQNLIKQ NCELFEQLGE
      HHHHHHHHHHH      HH      H      HHHHH HHHHHHHHHHH HHHHHHH

401  IX
      YKFQNALLVR YTKKVPQVST PTLVEVSRNL GKVGSKCCKH PEAKRMPCAE
      HHHHHHHHHHH HHHH      H HHHHHHHHHHH      HHH      HHHHHHHH

451  X          XI
      DYLSVVLNQL CVLHEKTPVS DRVTKCCTES LVNRRPPCFSA LEVDETYVPK
      HHHHHHHHHHH HHHHH      HHHHHHHHHH      HHHHHHHHH

501  EFNAETFTFH ADICTLSEKE RQIKKQTALV ELVKHKPKAT KEQLKAVMDD
      HHH      HHH HHHHMMEHHS HHH      HHHHHHHH

551  XII
      FAAFVEKCCK ADDKETCFAE EGKKLVAAASQ AALGL
      HHHHHHHH      HHHH HHHHHHHHHHH HH

```

## Loop

I Val54-Asn61  
 II Thr76-Asp89  
 III Ala92-Glu100  
 IV Gln170-Ala176  
 V His247-Glu252  
 VI Glu266-Glu277

## Loop

VII Glu280-His288  
 VIII Ala362-Glu368  
 IX Lys439-Pro447  
 X Val462-Lys475  
 XI Thr478-Pro486  
 XII Lys560-Thr566

# Figure 10

## a. Randomisation of Loop IV.

151    APELLFFAKR YKAAFTECCQ <sup>IV</sup>AADKAACLLP KLDEL RDEGK ASSAKQRLKC  
       HHHHHHHHHH HHHHHHHHHH       HHHHH HHHHHHHHHHH HHHHHHHHHHH

151    APELLFFAKR YKAAFTECCX <sup>IV</sup>XXXXXXXXCLLP KLDEL RDEGK ASSAKQRLKC  
       HHHHHHHHHH HHHHHHHHHH       HHHHH HHHHHHHHHHH HHHHHHHHHHH

**X** represents the mutation of the natural amino acid to any other amino acid. One, more or all of the amino acids can be changed in this manner. This figure indicates all the residues have been changed.

## b. Insertion (or replacement) of Randomised sequence into Loop IV.

(X)<sub>n</sub>



151    APELLFFAKR YKAAFTECCQ <sup>IV</sup>AADKAACLLP KLDEL RDEGK ASSAKQRLKC  
       HHHHHHHHHH HHHHHHHHHH       HHHHH HHHHHHHHHHH HHHHHHHHHHH

The insertion can be at any point on the loop and a length where n would typically be 6, 8, 12, 20 or 25.

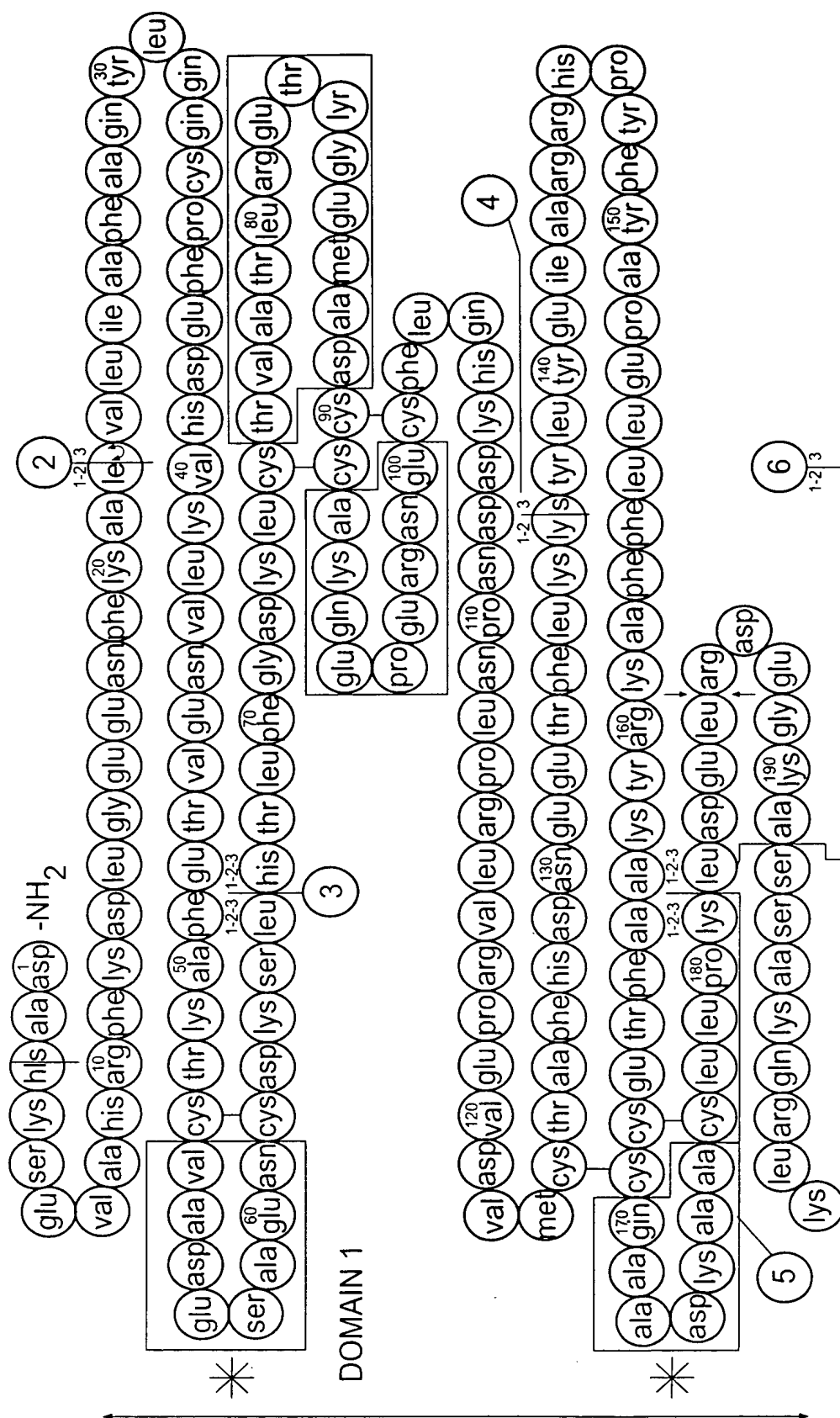


FIG. 11A

**FIG. 11B**

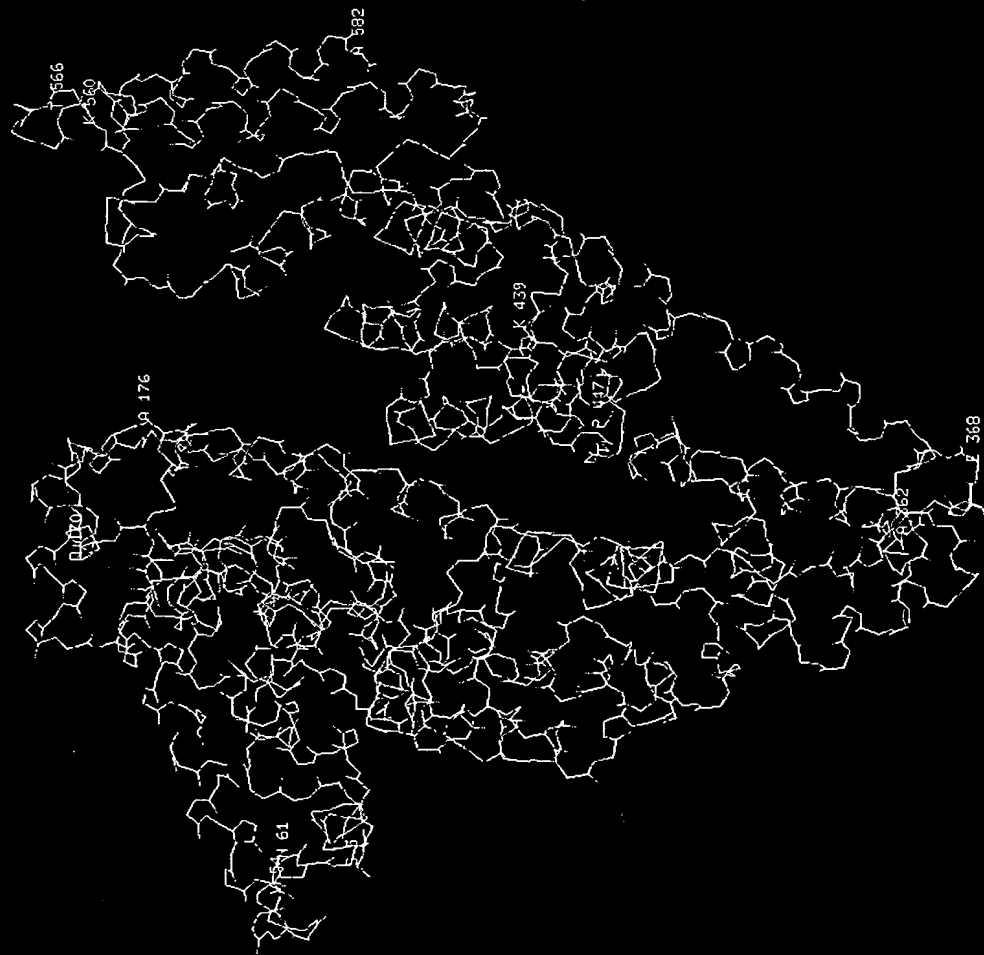
FROM FIG. 11B





1000 900 800 700 600 500 400 300 200 100 0

1X HSA (1147 x 894)



**FIG. 13**  
TERTIARY STRUCTURE OF HSA

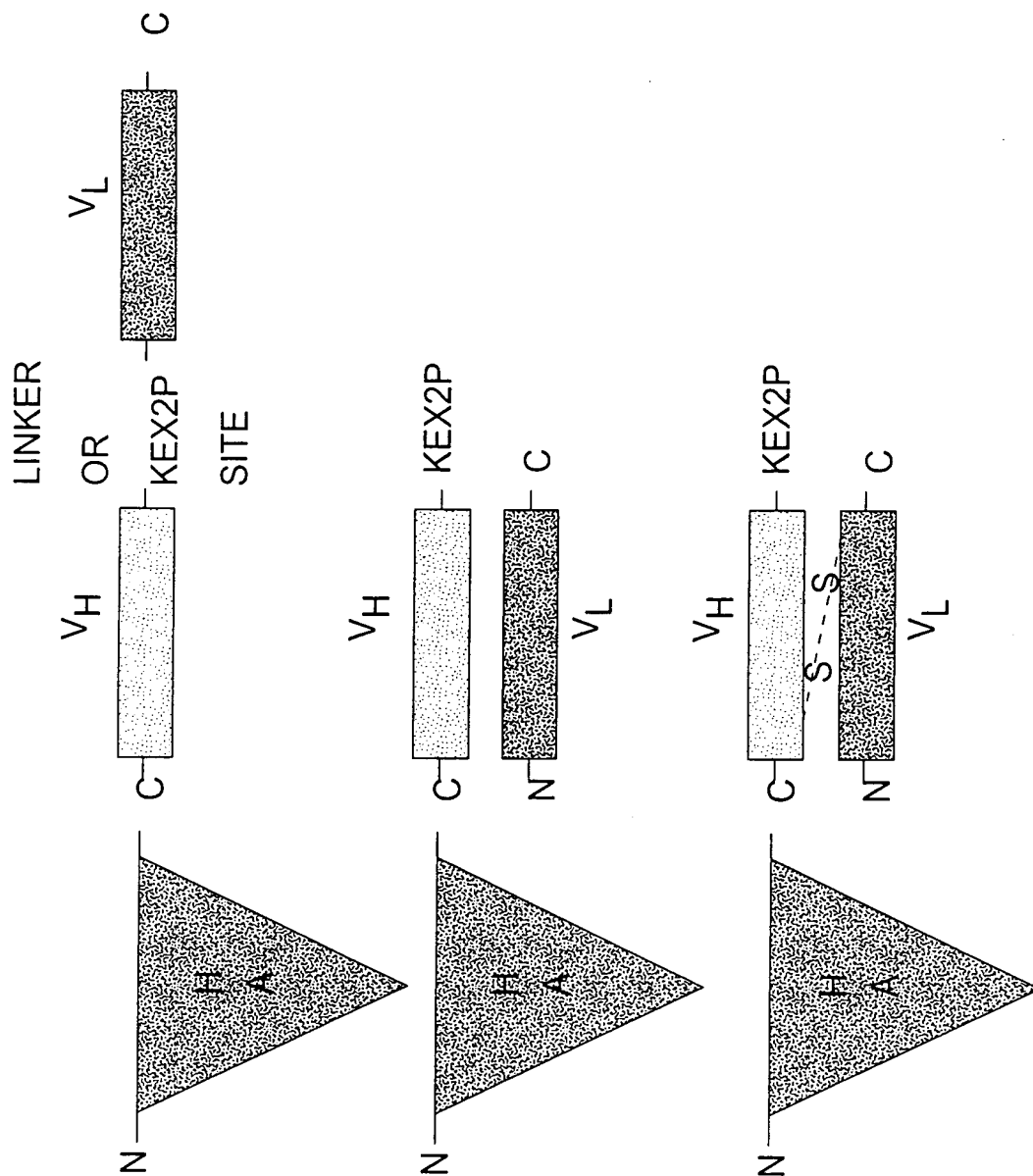


FIG. 14



1 GAT GCA CAC AAG AGT GAG GTT GCT CAT CGG TTT AAA GAT TTG GGA GAA AAT TTC AAA 60  
 1 D A H K S E V A H R F K D L G E N F K 20  
 61 GCC TTG GTG ATT GCC TTT GCT CAG TAT CTT CAG CAG TGT CCA TTT GAA GAT CAT GTA 120  
 21 A L V L I A F A Q Y L Q Q C P F E D H V 40  
 121 AAA TTA GTG AAT GAA GTA ACT GAA TTT GCA AAA ACA TGT GTT GCT GAT GAG TCA GCT GAA 180  
 41 K L V N E V T E F A K T C V A D E S A E 60  
 181 AAT TGT GAC AAA TCA CTT CAT ACC CTT TTT GGA GAC AAA TTA TGC ACA GTT GCA ACT CTT 240  
 61 N C D K S L H T L F G D K L C T V A T L 80  
 241 CGT GAA ACC TAT GGT GAA ATG GCT GAC TGC TGT GCA AAA CAA GAA CCT GAG AGA AAT GAA 300  
 81 R E T Y G E M A D C C A K Q E P E R N E 100  
 301 TGC TTC TTG CAA CAC AAA GAT GAC AAC CCA AAC CTC CCC CGA TTG GTG AGA CCA GAG GTT 360  
 101 C F L Q H K D D N P N L P R L V R P E V 120  
 361 GAT GTG ATG TGC ACT GCT TTT CAT GAC AAT GAA GAG ACA TTT TTG AAA AAA TAC TTA TAT 420  
 121 D V M C T A F H D N E E T F L K K Y L Y 140  
 421 GAA ATT GCC AGA AGA CAT CCT TAC TTT TAT GCC CCG GAA CTC CTT TTC TTT GCT AAA AGG 480  
 141 E I A R R H P Y F Y A P E L L F F A K R 160

Figure 15A

481 TAT AAA GCT GCT TTT ACA GAA TGT TGC CAA GCT GCT GAT AAA GCT GCC TGC CTG TTG CCA 540  
 161 Y K A A F T E C C Q A A D K A A C L L P 180

541 AAG CTC GAT GAA CTT CGG GAT GAA GGG AAG GCT TCG TCT GCC AAA CAG AGA CTC AAA TGT 600  
 181 K L D E L R D E G K A S S A K Q R L K C 200

601 GCC AGT CTC CAA AAA TTT GGA GAA AGA GCT TTC AAA GCA TGG GCA GTG GCT CGC CTG AGC 660  
 201 A S L Q K K F G E R A F K A W A V A R L S 220

661 CAG AGA TTT CCC AAA GCT GAG TTT GCA GAA GTT TCC AAG TTA GTG ACA GAT CTT ACC AAA 720  
 221 Q R F P K A E F A E V S K L V T D L T K 240

721 GTC CAC ACG GAA TGC TGC CAT GGA GAT CTG CTT GAA TGT GCT GAT GAC AGG GCG GAC CTT 780  
 241 V H T E C C H G D L L E C A D D R A D L 260

781 GCC AAG TAT ATC TGT GAA AAT CAG GAT TCG ATC TCC AGT AAA CTG AAG GAA TGC TGT GAA 840  
 261 A K Y I C E N Q D S I S S K L K E C C E 280

841 AAA CCT CTG TTG GAA AAA TCC CAC TGC ATT GCC GAA GTG GAA AAT GAT GAG ATG CCT GCT 900  
 281 K P L L E K S H C I A E V E N D E M P A 300

901 GAC TTG CCT TCA TTA GCT GCT GAT TTT GTT GAA AGT AAG GAT GTT TGC AAA AAC TAT GCT 960  
 301 D L P S L A A D F V E S K D V C K N Y A 320

Figure 15B

961	GAG	GCA	AAG	GAT	GTC	TTC	CTG	GGC	ATG	TTT	TTG	TAT	GAA	TAT	GCA	AGA	AGG	CAT	CCT	GAT	1020
321	E	A	K	D	V	F	L	G	M	F	L	Y	E	Y	A	R	R	H	P	D	340
1021	TAC	TCT	GTC	GTG	CTG	CTG	CTG	AGA	CTT	GCC	AAG	ACA	TAT	GAA	ACC	ACT	CTA	GAG	AAG	TGC	1080
341	Y	S	V	V	L	L	L	R	L	A	K	T	Y	E	T	T	L	E	K	C	360
1081	TGT	GCC	GCT	GCA	GAT	CCT	CAT	GAA	TGC	TAT	GCC	AAA	GTG	TTC	GAT	GAA	TTT	AAA	CCT	CTT	1140
361	C	A	A	A	D	P	H	E	C	Y	A	K	V	F	D	E	F	K	P	L	380
1141	GTG	GAA	GAG	CCT	CAG	AAT	TTA	ATC	AAA	CAA	AAC	TGT	GAG	CTT	TTT	GAG	CAG	CTT	GGA	GAG	1200
381	V	E	E	P	Q	N	L	I	K	Q	N	C	E	L	F	E	Q	L	G	E	400
1201	TAC	AAA	TTC	CAG	AAT	GCG	CTA	TTA	GTT	CGT	TAC	ACC	AAG	AAA	GTA	CCC	CAA	GTG	TCA	ACT	1260
401	Y	K	F	Q	N	A	L	L	V	R	Y	T	K	K	V	P	Q	V	S	T	420
1261	CCA	ACT	CTT	GTA	GAG	GTC	TCA	AGA	AAC	CTA	GGA	AAA	GTG	GGC	AGC	AAA	TGT	TGT	AAA	CAT	1320
421	P	T	L	V	E	V	S	R	N	L	G	K	V	G	S	K	C	C	K	H	440
1321	CCT	GAA	GCA	AAA	AGA	ATG	CCC	TGT	GCA	GAA	GAC	TAT	CTA	TCC	GTG	GTC	CTG	AAC	CAG	TTA	1380
441	P	E	A	K	R	M	P	C	A	E	D	Y	L	S	V	V	L	N	Q	L	460
1381	TGT	GTG	TTG	CAT	GAG	AAA	ACG	CCA	GTA	AGT	GAC	AGA	GTC	ACA	AAA	TGC	TGC	ACA	GAG	TCC	1440
461	C	V	L	H	E	K	T	P	V	S	D	R	V	T	K	C	C	T	E	S	480

**Figure 15C**

1441 TTG GTG AAC AGG CGA CCA TGC TTT TCA GCT CTG GAA GTC GAT GAA ACA TAC GTT CCC AAA 1500  
481 L V N R R R P C F S A L E V D E T Y V P K 500

1501 GAG TTT AAT GCT GAA ACA TTC ACC TTC CAT GAT ATA TGC ACA CTT TCT GAG AAG GAG 1560  
501 E F N A E T F T F H A D I C T L S E K E 520

1561 AGA CAA ATC AAG AAA CAA ACT GCA CTT GTT GAG CTT GTG AAA CAC AAG CCC AAG GCA ACA 1620  
521 R Q I K K Q T A L V E L V K H K P K A T 540

1621 AAA GAG CAA CTG AAA GCT GTT ATG GAT TTT GCA GCT TTT GTA GAG AAG TGC TGC AAG 1680  
541 K E Q L K A V M D D F A A F V E K C C K 560

1681 GCT GAC GAT AAG GAG ACC TGC TTT GCC GAG GGT AAA AAA CTT GTT GCT GCA AGT CAA 1740  
561 A D D K E T C F A E E G K K L V A A S Q 580

1741 GCT GCC TTA GGC TTA TAA CAT CTA CAT TTA AAA GCA TCT CAG 1782  
581 A A L G L \* 585

Figure 15D